

FIGURE 1

1 AGAAAGGGGT GCGGCAGCAC TGCCAGGGGA AGAGGGTGAT CCGACCCGGG
 51 GAAGGTCGCT GGGCAGGGCG AGTTGGGAAA GCGGCAGCCC CCGCCGCCCC
 101 CGCAGCCCCT TCTCCTCCTT TCTCCCACGT CCTATCTGCC TCTCGCTGGA
 151 GGCCAGGCCG TGCAGCATCG AAGACAGGAG GAACTGGAGC CTCATTGGCC
 201 GGCCCGGGGC GCCGGCCTCG GGCTTAAATA GGAGCTCCGG GCTCTGGCTG
 251 GGACCCGACC GCTGCCGGCC GCGCTCCCGC TGCTCCTGCC GGGTGATGGA
 301 AAACCCAGC CCGGCCGCCG CCCTGGGCAA GGCCCTCTGC GCTCTCCTCC
 351 TGGCCACTCT CGGCGCCGCC GGCCAGCCTC TTGGGGGAGA GTCCATCTGT
 401 TCCGCCGGAG CCCC GGCCAA ATACAGCATC ACCTTCACGG GCAAGTGGAG
 451 CCAGACGGCC TTCCCCAAGC AGTACCCCT GTTCCGCCCC CCTGCGCAGT
 501 GGTCTTCGCT GCTGGGGGCC GCGCATAGCT CCGACTACAG CATGTGGAGG
 551 AAGAACCAGT ACGTCAGTAA CGGGCTGCGC GACTTTGCGG AGCGCGGCGA
 601 GGCTGGGCG CTGATGAAGG AGATCGAGGC GGCGGGGGAG GCGCTGCAGA
 651 GCGTGCACGC GGTGTTTTTCG GCGCCCGCCG TCCCAGCGG CACCGGGCAG
 701 ACGTCGGCGG AGCTGGAGGT GCAGCGCAGG CACTCGCTGG TCTCGTTTGT
 751 GGTGCGCATC GTGCCAGCC CCGACTGGTT CGTGGGCGTG GACAGCCTGG
 801 ACCTGTGCGA CGGGGACCGT TGGCGGGAAC AGGCGGCGCT GGACCTGTAC
 851 CCCTACGACG CCGGGACGGA CAGCGGCTTC ACCTTCTCCT CCCCCAACTT
 901 CGCCACCATC CCGCAGGACA CCGTGACCGA GATAACGTCC TCCTCTCCCA
 951 GCCACCCGGC CAACTCCTTC TACTACCCAC GGCTGAAGGC CCTGCCTCCC
 1001 ATCGCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCCA GGGCCTTCAT
 1051 CCCTCCCGCC CCAGTCCTGC CCAGCAGGGA CAATGAGATT GTAGACAGCG
 1101 CCTCAGTTCC AGAAACGCCG CTGGACTGCG AGGTCTCCCT GTGGTCGTCC
 1151 TGGGGACTGT GCGGAGGCCA CTGTGGGAGG CTCGGGACCA AGAGCAGGAC
 1201 TCGCTACGTC CGGGTCCAGC CCGCCAACAA CGGGAGCCCC TGCCCCGAGC
 1251 TCGAAGAAGA GGCTGAGTGC GTCCCTGATA ACTGCGTCTA AGACCAGAGC

FIGURE 1 - continued

1301 CCCGCAGCCC CTGGGGCCCC CCGGAGCCAT GGGGTGTCGG GGGCTCCTGT
1351 GCAGGCTCAT GCTGCAGGCG GCCGAGGGCA CAGGGGGTTT CGCGCTGCTC
1401 CTGACCGCGG TGAGGCCGCG CCGACCATCT CTGCACTGAA GGGCCCTCTG
1451 GTGGCCGGCA CGGGCATTGG GAAACAGCCT CCTCCTTTCC CAACCTTGCT
1501 TCTTAGGGGC CCCC GTGTCC CGTCTGCTCT CAGCCTCCTC CTCCTGCAGG
1551 ATAAAGTCAT CCCC AAGGCT CCAGCTACTC TAAATTATGT CTCCTTATAA
1601 GTTATTGCTG CTCCAGGAGA TTGTCCTTCA TCGTCCAGGG GCCTGGCTCC
1651 CACGTGGTTG CAGATACCTC AGACCTGGTG CTCTAGGCTG TGCTGAGCCC
1701 ACTCTCCCGA GGGCGCATCC AAGCGGGGGC CACTTGAGAA GTGAATAAAT
1751 GGGGCGGTTT CGGAAGCGTC

FIGURE 2

1 MENPSPAAAL GKALCALLLA TLGAAGQPLG GESICSAGAP AKYSITFTGK
51 WSOTAFPKOY PLFRPPAOWS SLLGAAHSSD YSMWRKNOYV SNGLRDFAER
101 GEAWALMKEI EAAGEALQSV HAVFSAPAVP SGTGQTS AEL EVORRHSLVS
151 FVVRIVSPD WFGVDSL DL CDGDRWREOA ALDLYPYDAG TDSGFTFSSP
201 NFATIPQDTV TEITSSSPSH PANSFYYPRL KALPPIARVT LVRLRQSPRA
251 FIPPAPVLPS RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGR LGTKS
301 RTRYVRVOPA NNGSPCPELE EEAECVPDNC V

FIGURE 3

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RG1      1 MENPSPAAALGKALCALLLATLGA.AGQPLGGESICSAGAPAKYSITFTG 49
          ||| | . | : | ||| ||. ||||| |||:|. | |:|||||
mindin 1 MENVS..FSLDRTLWVFLAMLGSTAGQPLGGESVCTARPLARYSITFTG 48

          50 KWSQTAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAE 99
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          49 KWSQTAFPKQYPLFRPPAQWSSLLGAAHSSDYSMWRKNEYVSNGLRDFAE 98

          100 RGEAWALMKEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLV 149
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          99 RGEAWALMKEIEAAGEKLQSVHAVFSAPAVPSGTGQTSAELEVHPRHSLV 148

          150 SFVVRIVPSPDWVFGVDSLDCGDRWREQAALDLYPYDAGTDSGFTFSS 199
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          149 SFVVRIVPSPDWVFGIDSLDCEGGRWKEQVVDLYPHDAGTDSGFTFSS 198

          200 PNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLVRLRQSPR 249
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          199 PNFATIPQDTVTEITASSPSHPANSFYYPRLKSLPPIAKVTFVRLRQSPR 248

          250 AFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTK 299
          || ||. | || ||||| ||||| ||||| ||||| ||||| |||||
          249 AFAPPSLDLASRGNEIVDSLSPETPLDCEVSLWSSWGLCGGPCGKLGAK 298

          300 SRTRYVRVQPANNGSPCPELEEEAECVPDNCV 331
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
          299 SRTRYVRVQPANNGTPCPELEEEAECAPDNCV 330

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FIGURE 4

AGAAAGGGGTGCGGCAGCACTGCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTGCT
 1 -----+-----+-----+-----+-----+ 60
 TCTTTCCCCACGCCGTCGTGACGGTCCCTTCTCCCACTAGGCTGGGCCCTTCCAGCGA

 GGGCAGGGCGAGTTGGGAAAGCGGCAGCCCCCGCCGCCCGCAGCCCCCTTCTCCTCCTT
 61 -----+-----+-----+-----+-----+ 120
 CCCGTCCCGCTCAACCTTTTCGCCGTGCGGGGCGCGGGGGCGTCGGGAAGAGGAGGAA

 TCTCCACGTCCTATCTGCCTCTCGCTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAG
 121 -----+-----+-----+-----+-----+ 180
 AGAGGGTGACAGATAGACGGAGAGCGACCTCCGGTCCGGCACGTCGTAGCTTCTGTCTC

 GAACTGGAGCCTCATTGGCCGGCCCCGGGGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGG
 181 -----+-----+-----+-----+-----+ 240
 CTTGACCTCGGAGTAACCGGCCGGGGCCCCGCGGCCGGAGCCCGAATTTATCCTCGAGGCC

 GCTCTGGCTGGGACCCGACCGCTGCCGGCCGCGCTCCCGCTGCTCCTGCCGGGTGATGGA
 241 -----+-----+-----+-----+-----+ 300
 CGAGACCGACCTGGGCTGGCGACGGCCGGCGGAGGGCGACGAGGACGGCCCCACTACCT

 b M E -
 AAACCCAGCCCGGCCGCCCTGGGCAAGGCCCTCTGCGCTCTCCTCCTGGCCACTCT
 301 -----+-----+-----+-----+-----+ 360
 TTTGGGGTCCGGCCGGCGGGACCCGTTCGGGAGACGCGAGAGGAGGACCGGTGAGA

 b N P S P A A A L G K A L C A L L L A T L -
 CGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTCCATCTGTTCCGCCGGAGCCCCGGCCAA
 361 -----+-----+-----+-----+-----+ 420
 GCCGCGCGGCCGGTCCGAGAACCCCTCTCAGGTAGACAAGGCGGCCTCGGGGCCGGTT

 b G A A G Q P L G G E S I C S A G A P A K -
 ATACAGCATCACCTTCACGGGCAAGTGGAGCCAGACGGCCTTCCCCAAGCAGTACCCCT
 421 -----+-----+-----+-----+-----+ 480
 TATGTCGTAGTGGAAGTGCCCGTTACCTCGGTCTGCCGGAAGGGTTTCGTCATGGGGGA

 b Y S I T F T G K W S Q T A F P K Q Y P L -
 GTTCCGCCCCCTGCGCAGTGGTCTTCGCTGCTGGGGGCGCGCATAGCTCCGACTACAG
 481 -----+-----+-----+-----+-----+ 540
 CAAGGCGGGGGACGCGTCACCAGAAGCGACGACCCCGGCGGTATCGAGGCTGATGTC

 b F R P P A Q W S S L L G A A H S S D Y S -
 CATGTGGAGGAAGAACCAGTACGTACGTAACGGGCTGCGCGACTTTGCGGAGCGCGGCGA
 541 -----+-----+-----+-----+-----+ 600
 GTACACCTCCTTCTTGGTCATGCAGTCATTGCCCGACGCGCTGAAACGCCTCGCGCCGCT

 b M W R K N Q Y V S N G L R D F A E R G E -

FIGURE 4 - continued

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GGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGAGGCGCTGCAGAGCGTGACACGC
601 -----+-----+-----+-----+-----+-----+ 660
CCGGACCCGCGACTACTTCCTCTAGCTCCGCCGCCCCCTCCGCGACGTCTCGCACGTGCG

b      A W A L M K E I E A A G E A L Q S V H A -

GGTGTTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGGGCAGACGTCCGGCGGAGCTGGAGGT
661 -----+-----+-----+-----+-----+-----+ 720
CCACAAAAGCCGCGGGCGGCAGGGGTGCGCGTGGCCCGTCTGCAGCCGCCTCGACCTCCA

b      V F S A P A V P S G T G Q T S A E L E V -

GCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCCCAGCCCCGACTGGTT
721 -----+-----+-----+-----+-----+-----+ 780
CGTCGCGTCCGTGAGCGACAGAGCAAACACCACGCGTAGCACGGGTCTGGGGTCTGACCAA

b      Q R R H S L V S F V V R I V P S P D W F -

CGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGGAACAGGCGGCGCT
781 -----+-----+-----+-----+-----+-----+ 840
GCACCCGCACCTGTGCGACCTGGACACGCTGCCCTGGCAACCGCCCTTGTCGCCGCCGA

b      V G V D S L D L C D G D R W R E Q A A L -

GGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCCTCCCCAACTT
841 -----+-----+-----+-----+-----+-----+ 900
CCTGGACATGGGGATGCTGCGGCCCTGCCTGTGCGCGAAGTGGAAGAGGAGGGGGTTGAA

b      D L Y P Y D A G T D S G F T F S S P N F -

CGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCAGCCACCCGGC
901 -----+-----+-----+-----+-----+-----+ 960
GCGGTGGTAGGGCGTCTGTGCCACTGGCTCTATTGCAGGAGGAGAGGGTCTGGTGGGCCG

b      A T I P Q D T V T E I T S S S P S H P A -

CAACTCCTTCTACTACCCACGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGACACTGGT
961 -----+-----+-----+-----+-----+-----+ 1020
GTTGAGGAAGATGATGGGTGCCGACTTCCGGGACGGAGGGTAGCGGTCCCACTGTGACCA

b      N S F Y Y P R L K A L P P I A R V T L V -

GCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGCAGGGA
1021 -----+-----+-----+-----+-----+-----+ 1080
CGCCGACGCTGTCTCGGGGTCCCGGAAGTAGGGAGGGCGGGGTCTAGGACGGGTCTGCCCT

b      R L R Q S P R A F I P P A P V L P S R D -

CAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTCCCT
1081 -----+-----+-----+-----+-----+-----+ 1140
GTTACTCTAACATCTGTGCGGAGTCAAGGTCTTTGCGGCGACCTGACGCTCCAGAGGGA

b      N E I V D S A S V P E T P L D C E V S L -

```

FIGURE 4 - continued

1141 GTGGTCGTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGAC 1200
 -----+-----+-----+-----+-----+
 CACCAGCAGGACCCCTGACACGCCTCCGGTGACACCCCTCCGAGCCCTGGTTCTCGTCCTG
 b W S S W G L C G G H C G R L G T K S R T -

1201 TCGCTACGTCCGGGTCCAGCCCCGCAACAACGGGAGCCCCTGCCCCGAGCTCGAAGAAGA 1260
 -----+-----+-----+-----+-----+
 AGCGATGCAGGCCAGGTGCGGGCGGTTGTTGCCCTCGGGGACGGGGCTCGAGCTTCTTCT

b R Y V R V Q P A N N G S P C P E L E E E -

1261 GGCTGAGTGCGTCCCTGATAACTGCGTCTAAGACCAGAGCCCCGAGCCCCCTGGGGCCCC 1320
 -----+-----+-----+-----+-----+
 CCGACTCACGCAGGGACTATTGACGCAGATTCTGGTCTCGGGGCGTCGGGGACCCCCGGG

b A E C V P D N C V * -

1321 CCGGAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCA 1380
 -----+-----+-----+-----+-----+
 GGCTTCGGTACCCACAGCCCCGAGGACACGTCCGAGTACGACGTCCGCCGGCTCCCGT

1381 CAGGGGGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAA 1440
 -----+-----+-----+-----+-----+
 GTCCCCCAAAGCGCGACGAGGACTGGCGCCACTCCGGCGCGGCTGGTAGAGACGTGACTT

1441 GGGCCCTCTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTCCCAACCTTGCT 1500
 -----+-----+-----+-----+-----+
 CCCGGGAGACCACCGGCCGTGCCCGTAACCCTTTGTGCGGAGGAGGAAAGGTTGGAACGA

1501 TCTTAGGGGCCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCAT 1560
 -----+-----+-----+-----+-----+
 AGAATCCCCGGGGGCACAGGGCAGACGAGAGTCGGAGGAGGAGGACGTCCCTATTTTCAGTA

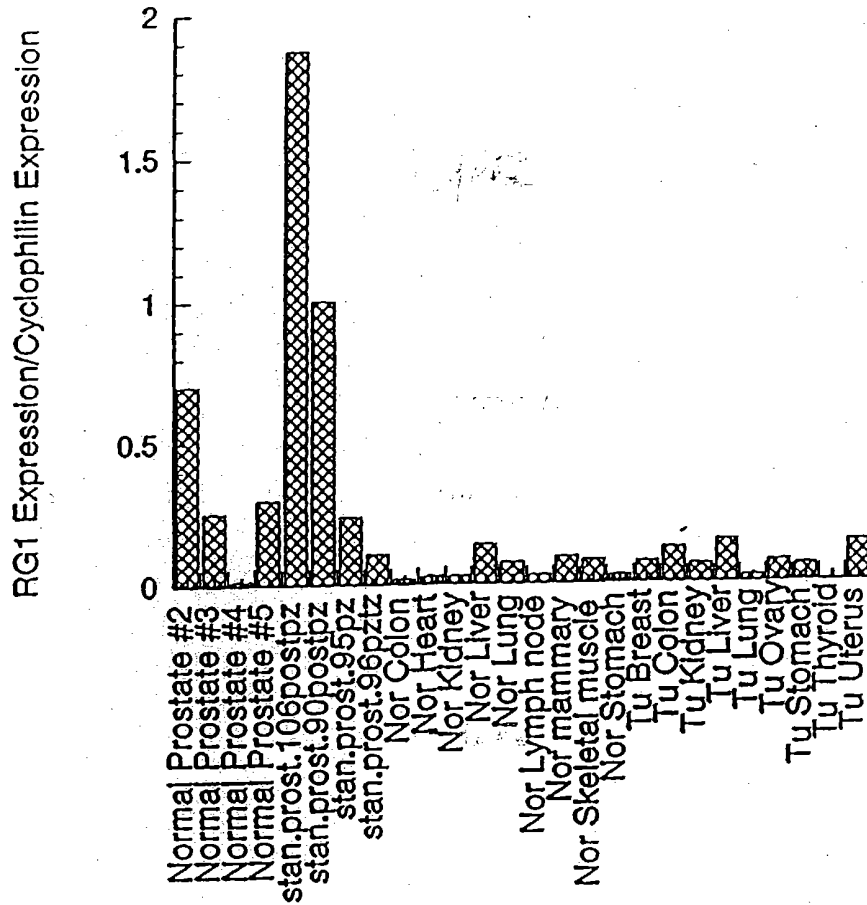
1561 CCCCCAAGGCTCCAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGA 1620
 -----+-----+-----+-----+-----+
 GGGGTTCGAGGTGATGAGATTTAATACAGAGGAATATTCAATAACGACGAGGTCTCT

1621 TTGTCCCTTCATCGTCCAGGGGCTGGCTCCACGTGGTTGCAGATACCTCAGACCTGGTG 1680
 -----+-----+-----+-----+-----+
 AACAGGAAGTAGCAGGTCCCCGACCGAGGGTGACCAACGTCTATGGAGTCTGGACCAC

1681 CTCTAGGCTGTGCTGAGCCCACTCTCCCGAGGGGCGCATCCAAGCGGGGGCCACTTGAGAA 1740
 -----+-----+-----+-----+-----+
 GAGATCCGACACGACTCGGGTGAGAGGGCTCCCGGTAGGTTGCCCCCGGTGAACTCTT

1741 GTGAATAAATGGGGCGGTTTCGGAAGCGTC 1770
 -----+-----+-----+
 CACTTATTTACCCCGCCAAAGCCTTCGCAG

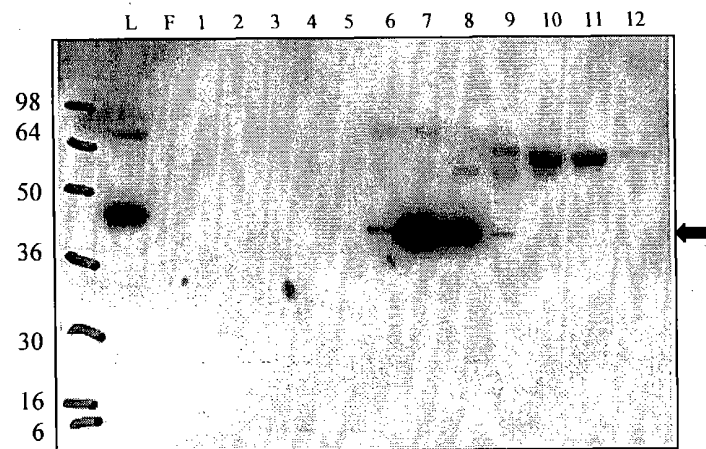
FIGURE 5

Expression of *Rg1* mRNA in human tissues

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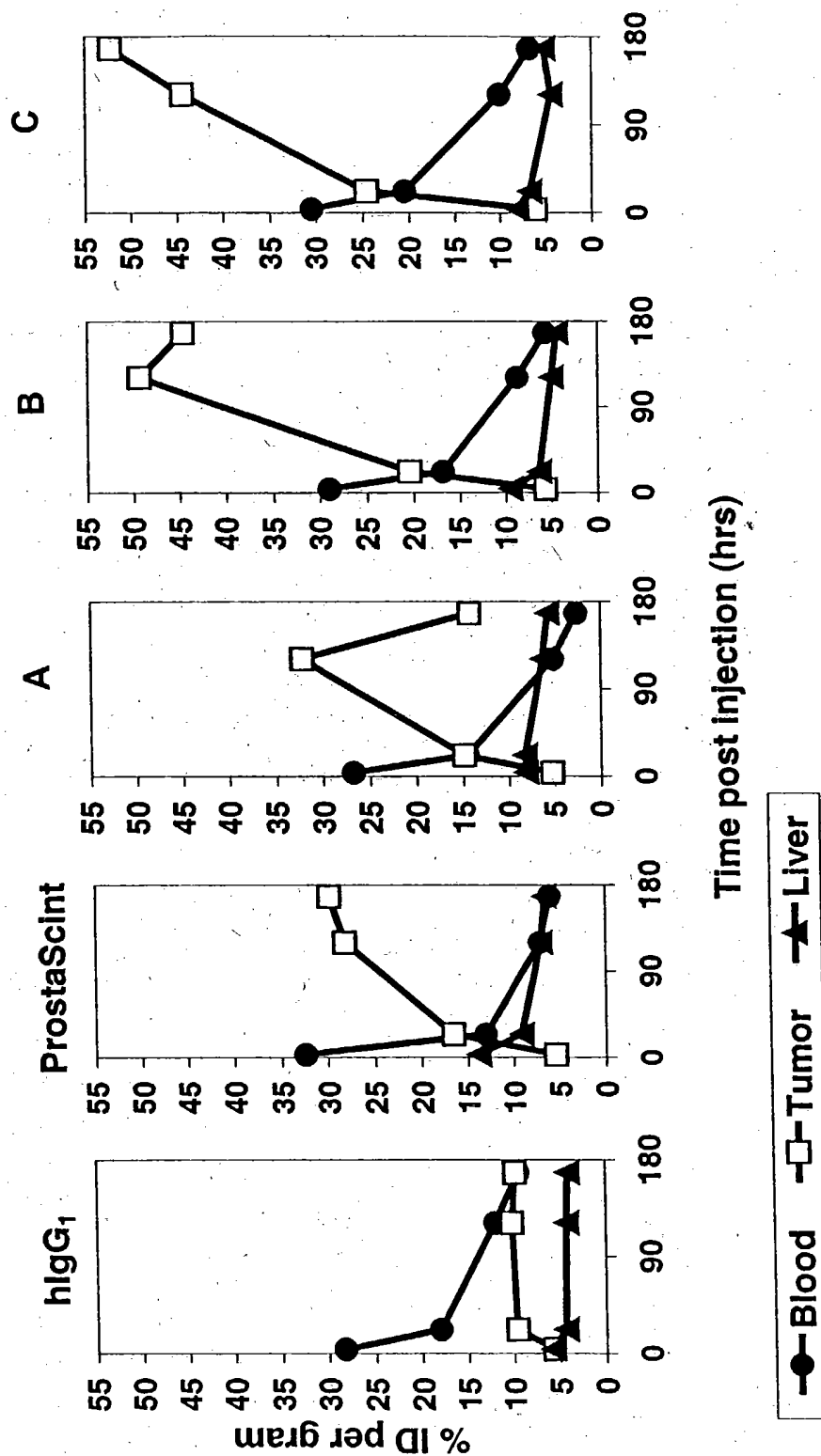
FIGURE 6

Purification of Native RG1 Protein Secreted
by LNCaP Cells.



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FIGURE 7



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FIGURE 8

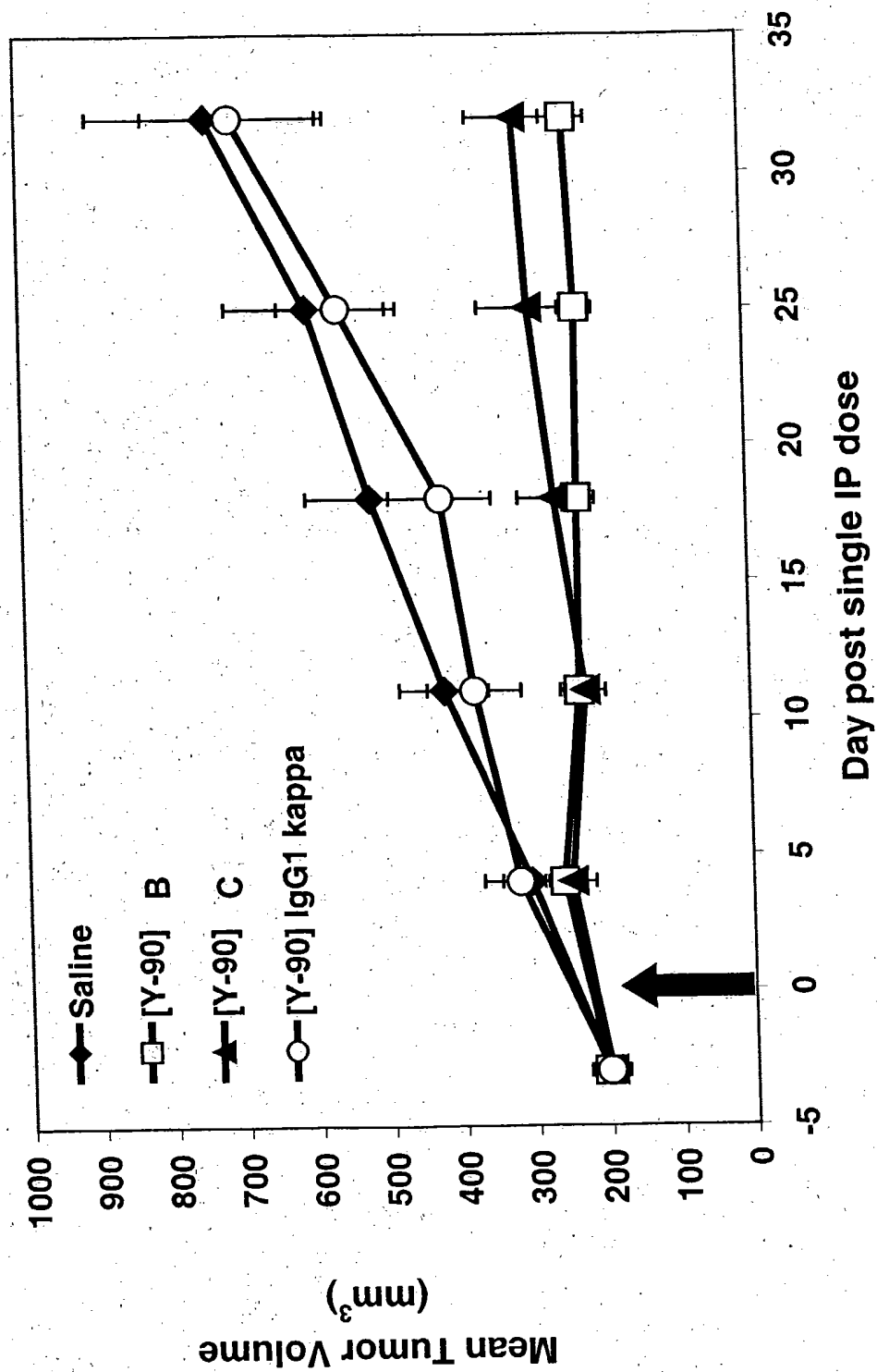


FIGURE 9

huMAb B Variable Region Sequences

 V_L

1 METPAQLLFLLLLWLPD~~TT~~GEIVLTQSPGTL~~SL~~SPGERATL~~SC~~RASQSVS 50

51 SSYLAWYQQKPGQAPRL~~LI~~YGASSRATGIPDRFSGSGSGTDFTLTISRLE 100

101 PEDFAVYYCQ~~QY~~SSSLTFGGGTKVEIK 150

 V_H

1 MEFVLSWVFLVAILKGVQCEVQLVQSGGGLVHPGGSRLRLSCAGSGGFTFSS 50

51 YVMHWLRQAPGKGLEWVSVIGTGGVTHYADSVKGRFTISRDNAKNSLYLQ 100

101 MNSLRAEDMAMYYCARWGY~~YG~~SGSYENDAFDIWGQGTMTVTVSSASTK 150

B_{3M}, V_H (mutations in bold)

1 MEFVLSWVFLVAILKGVQCEVQLVQSGGGLVQPGGSRLRLSCAGSGGFTFSS 50

51 YVMHWLRQAPGKGLEWVSVIGTGGVTHYADSVKGRFTISRDNAKNSLYLQ 100

101 MNSLRAEDTAVYYCARWGY~~YG~~SGSYENDAFDIWGQGTMTVTVSSASTK 150

CDR sequences (1,2,and 3)for each variable region are underlined

FIGURE 10

HuMAb C Variable Region Sequences

 V_L

1 METPAQLLFLLLLWLPD TTGEIVLTQSPG TSLSPGERATLSCRASQSVS 50
 51 SSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLE 100
 101 PEDFAVYYCQQYGSSLTFGGGTKVEIK 150

 V_H

1 MEFVLSWVFLVAILKGVQCEVQLVQSGGGLVHPGGSLRLSCAGSGFTFSS 50
 51 YVMHWVRQAPGKGLEWVSVIGTGGVTNYADSVKGRFTISRDN AKNSLYLQ 100
 101 MNSLRAEDMAVYYCARWGDWDDAFDIWGQGTMTVTVSSASTK 144

 C_{2m}, V_H

(mutations in bold)

1 MEFVLSWVFLVAILKGVQCEVQLVQSGGGLV**Q**PGGSLRLSCAGSGFTFSS 50
 51 YVMHWVRQAPGKGLEWVSVIGTGGVTNYADSVKGRFTISRDN AKNSLYLQ 100
 101 MNSLRAEDTAVYYCARWGDWDDAFDIWGQGTMTVTVSSASTK 144

CDR sequences (CDR 1,2, and 3) for each variable region are underlined